

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/511,832

Source: P4710

Date Processed by STIC: 10/29/04

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 10/29/2004

PATENT APPLICATION: US/10/511,832

TIME: 11:33:33

Input Set : A:\ISIS0048-100.SEQ.txt

Output Set: N:\CRF4\10292004\J511832.raw

```

4 <110> APPLICANT: Susan M. Freier
6 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HYDROXYSTEROID
7     11-BETA DEHYDROGENASE 1 EXPRESSION
10 <130> FILE REFERENCE: RTS-0428
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/511,832
C--> 12 <141> CURRENT FILING DATE: 2004-10-19
12 <160> NUMBER OF SEQ ID NOS: 122
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Antisense Oligonucleotide
24 <400> SEQUENCE: 1
25 tccgtcatcg ctcttcaggg                20
27 <210> SEQ ID NO: 2
28 <211> LENGTH: 20
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
36 atgcattctg cccccaagga                20
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 1375
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (95)...(973)
47 <400> SEQUENCE: 3
48 attcagaggc tgctgcctgc ttaggaggtt gtagaaagct ctgtaggttc tctctgtgtg 60
49 tcttacagga gtcttcaggc cagctccctg tcgg atg gct ttt atg aaa aaa tat 115
50                                     Met Ala Phe Met Lys Lys Tyr
51                                     1               5
53 ctc ctc ccc att ctg ggg ctc ttc atg gcc tac tac tac tat tct gca 163
54 Leu Leu Pro Ile Leu Gly Leu Phe Met Ala Tyr Tyr Tyr Tyr Ser Ala
55      10               15               20
57 aac gag gaa ttc aga cca gag atg ctc caa gga aag aaa gtg att gtc 211
58 Asn Glu Glu Phe Arg Pro Glu Met Leu Gln Gly Lys Lys Val Ile Val
59      25               30               35
61 aca ggg gcc agc aaa ggg atc gga aga gag atg gct tat cat ctg gcg 259

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```

62 Thr Gly Ala Ser Lys Gly Ile Gly Arg Glu Met Ala Tyr His Leu Ala
63 40 45 50 55
65 aag atg gga gcc cat gtg gtg gtg aca gcg agg tca aaa gaa act cta 307
66 Lys Met Gly Ala His Val Val Val Thr Ala Arg Ser Lys Glu Thr Leu
67 60 65 70
69 cag aag gtg gta tcc cac tgc ctg gag ctt gga gca gcc tca gca cac 355
70 Gln Lys Val Val Ser His Cys Leu Glu Leu Gly Ala Ala Ser Ala His
71 75 80 85
73 tac att gct ggc acc atg gaa gac atg acc ttc gca gag caa ttt gtt 403
74 Tyr Ile Ala Gly Thr Met Glu Asp Met Thr Phe Ala Glu Gln Phe Val
75 90 95 100
77 gcc caa gca gga aag ctc atg gga gga cta gac atg ctc att ctc aac 451
78 Ala Gln Ala Gly Lys Leu Met Gly Gly Leu Asp Met Leu Ile Leu Asn
79 105 110 115
81 cac atc acc aac act tct ttg aat ctt ttt cat gat gat att cac cat 499
82 His Ile Thr Asn Thr Ser Leu Asn Leu Phe His Asp Asp Ile His His
83 120 125 130 135
85 gtg cgc aaa agc atg gaa gtc aac ttc ctc agt tac gtg gtc ctg act 547
86 Val Arg Lys Ser Met Glu Val Asn Phe Leu Ser Tyr Val Val Leu Thr
87 140 145 150
89 gta gct gcc ttg ccc atg ctg aag cag agc aat gga agc att gtt gtc 595
90 Val Ala Ala Leu Pro Met Leu Lys Gln Ser Asn Gly Ser Ile Val Val
91 155 160 165
93 gtc tcc tct ctg gct ggg aaa gtg gct tat cca atg gtt gct gcc tat 643
94 Val Ser Ser Leu Ala Gly Lys Val Ala Tyr Pro Met Val Ala Ala Tyr
95 170 175 180
97 tct gca agc aag ttt gct ttg gat ggg ttc ttc tcc tcc atc aga aag 691
98 Ser Ala Ser Lys Phe Ala Leu Asp Gly Phe Phe Ser Ser Ile Arg Lys
99 185 190 195
101 gaa tat tca gtg tcc agg gtc aat gta tca atc act ctc tgt gtt ctt 739
102 Glu Tyr Ser Val Ser Arg Val Asn Val Ser Ile Thr Leu Cys Val Leu
103 200 205 210 215
105 ggc ctc ata gac aca gaa aca gcc atg aag gca gtt tct ggg ata gtc 787
106 Gly Leu Ile Asp Thr Glu Thr Ala Met Lys Ala Val Ser Gly Ile Val
107 220 225 230
109 cat atg caa gca gct cca aag gag gaa tgt gcc ctg gag atc atc aaa 835
110 His Met Gln Ala Ala Pro Lys Glu Glu Cys Ala Leu Glu Ile Ile Lys
111 235 240 245
113 ggg gga gct ctg cgc caa gaa gaa gtg tat tat gac agc tca ctc tgg 883
114 Gly Gly Ala Leu Arg Gln Glu Glu Val Tyr Tyr Asp Ser Ser Leu Trp
115 250 255 260
117 acc act ctt ctg atc aga aat cca tgc agg aag atc ctg gaa ttt ctc 931
118 Thr Thr Leu Leu Ile Arg Asn Pro Cys Arg Lys Ile Leu Glu Phe Leu
119 265 270 275
121 tac tca acg agc tat aat atg gac aga ttc ata aac aag tag 973
122 Tyr Ser Thr Ser Tyr Asn Met Asp Arg Phe Ile Asn Lys *
123 280 285 290
125 gaactccctg agggctgggc atgctgaggg attttgggac tgttctgtct catgtttatc 1033
126 tgagctctta tctatgaaga catcttccca gagtgtcccc agagacatgc aagtcatggg 1093

```

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127 tcacacctga caaatggaag gagttcctct aacatttgca aaatggaaat gtaataataa 1153
128 tgaatgtcat gcaccgctgc agccagcagt tgtaaaattg ttagtaaaca taggtataat 1213
129 taccagatag ttatattaaa tttatatctt atatataata atatgtgatg attaatacaa 1273
130 tattaattat aataaaggtc acataaactt tataaattca taactggtag ctataacttg 1333
131 agcttattca ggatggttct ttaaaccata aactgtacaa tg 1375
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 24
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: PCR Primer
141 <400> SEQUENCE: 4
142 gtttctggga tagtccatat gcaa 24
144 <210> SEQ ID NO: 5
145 <211> LENGTH: 21
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: PCR Primer
152 <400> SEQUENCE: 5
153 agctccccct ttgatgatct c 21
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 25
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: PCR Probe
163 <400> SEQUENCE: 6
164 cagctccaaa ggaggaatgt gccct 25
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 19
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: PCR Primer
175 <400> SEQUENCE: 7
176 gaaggtgaag gtcggagtc 19
178 <210> SEQ ID NO: 8
179 <211> LENGTH: 20
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: PCR Primer
187 <400> SEQUENCE: 8
188 gaagatggtg atgggatttc 20
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 20
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence

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```

195 <220> FEATURE:
196 <223> OTHER INFORMATION: PCR Probe
198 <400> SEQUENCE: 9
199 caagcttccc gttctcagcc 20
201 <210> SEQ ID NO: 10
202 <211> LENGTH: 1350
203 <212> TYPE: DNA
204 <213> ORGANISM: Mus musculus
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (128)...(1006)
210 <400> SEQUENCE: 10
211 ggatgagaca gaaggataga gaggaggaga gagagagaga gaagagaagc aaccagaaat 60
212 aggcagccaa taaaaaggag cgcacttat ctgaagcctc aaggggcctg agccagggtcc 120
213 ctgtttg atg gca gtt atg aaa aat tac ctc ctc ccg atc ctg gtg ctc 169
214 Met Ala Val Met Lys Asn Tyr Leu Leu Pro Ile Leu Val Leu
215 1 5 10
217 tcc ctg gcc tac tac tac tat tct aca aat gaa gag ttc aga cca gaa 217
218 Ser Leu Ala Tyr Tyr Tyr Tyr Ser Thr Asn Glu Glu Phe Arg Pro Glu
219 15 20 25 30
221 atg ctc cag gga aag aaa gtg att gtc act ggg gcc agc aaa ggg att 265
222 Met Leu Gln Gly Lys Lys Val Ile Val Thr Gly Ala Ser Lys Gly Ile
223 35 40 45
225 gga aga gaa atg gca tat cat ctg tca aaa atg gga gcc cat gtg gta 313
226 Gly Arg Glu Met Ala Tyr His Leu Ser Lys Met Gly Ala His Val Val
227 50 55 60
229 ttg act gcc agg tcg gag gaa ggt ctc cag aag gta gtg tct cgc tgc 361
230 Leu Thr Ala Arg Ser Glu Glu Gly Leu Gln Lys Val Val Ser Arg Cys
231 65 70 75
233 ctt gaa ctc gga gca gcc tct gct cac tac att gct ggc act atg gaa 409
234 Leu Glu Leu Gly Ala Ala Ser Ala His Tyr Ile Ala Gly Thr Met Glu
235 80 85 90
237 gac atg aca ttt gcg gag caa ttt att gtc aag gcg gga aag ctc atg 457
238 Asp Met Thr Phe Ala Glu Gln Phe Ile Val Lys Ala Gly Lys Leu Met
239 95 100 105 110
241 ggc gga ctg gac atg ctt att cta aac cac atc act cag acc tcg ctg 505
242 Gly Gly Leu Asp Met Leu Ile Leu Asn His Ile Thr Gln Thr Ser Leu
243 115 120 125
245 tct ctc ttc cat gac gac atc cac tct gtg cga aga gtc atg gag gtc 553
246 Ser Leu Phe His Asp Asp Ile His Ser Val Arg Arg Val Met Glu Val
247 130 135 140
249 aac ttc ctc agc tac gtg gtc atg agc aca gcc gcc ttg ccc atg ctg 601
250 Asn Phe Leu Ser Tyr Val Val Met Ser Thr Ala Ala Leu Pro Met Leu
251 145 150 155
253 aag cag agc aat ggc agc att gcc gtc atc tcc tcc ttg gct ggg aaa 649
254 Lys Gln Ser Asn Gly Ser Ile Ala Val Ile Ser Ser Leu Ala Gly Lys
255 160 165 170
257 atg acc cag cct atg att gct ccc tac tct gca agc aag ttt gct ctg 697
258 Met Thr Gln Pro Met Ile Ala Pro Tyr Ser Ala Ser Lys Phe Ala Leu

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```

259 175          180          185          190
261 gat ggg ttc ttt tcc acc att aga aca gaa ctc tac ata acc aag gtc 745
262 Asp Gly Phe Phe Ser Thr Ile Arg Thr Glu Leu Tyr Ile Thr Lys Val
263          195          200          205
265 aac gtg tcc atc act ctc tgt gtc ctt ggc ctc ata gac aca gaa aca 793
266 Asn Val Ser Ile Thr Leu Cys Val Leu Gly Leu Ile Asp Thr Glu Thr
267          210          215          220
269 gct atg aag gaa atc tct ggg ata att gac gcc cta gct tct ccc aag 841
270 Ala Met Lys Glu Ile Ser Gly Ile Ile Asp Ala Leu Ala Ser Pro Lys
271          225          230          235
273 gag gag tgc gcc ctg gag atc atc aaa ggc aca gct cta cgc aaa agc 889
274 Glu Glu Cys Ala Leu Glu Ile Ile Lys Gly Thr Ala Leu Arg Lys Ser
275          240          245          250
277 gag gtg tac tat gac aaa ttg cct ttg act cca atc ctg ctt ggg aac 937
278 Glu Val Tyr Tyr Asp Lys Leu Pro Leu Thr Pro Ile Leu Leu Gly Asn
279 255          260          265          270
281 cca gga agg aag atc atg gaa ttt ttt tca tta cga tat tat aat aag 985
282 Pro Gly Arg Lys Ile Met Glu Phe Phe Ser Leu Arg Tyr Tyr Asn Lys
283          275          280          285
285 gac atg ttt gta agt aac tag gaactcctga gccctgggtga gtggtcttag 1036
286 Asp Met Phe Val Ser Asn *
287          290
289 aacagtctctg cctcatactt cagtaagccc taccacacaaa agtatctttc cagagataca 1096
290 caaatttttg ggtacacctc atcatgagaa attcttgcaa cacttgca ca gtgaaaatgt 1156
291 aattgtaata aatgtcacia accacttttg gcctgcagtt gtgaacttga ttgtaactat 1216
292 ggatataaac acatagtggg tgtatcgggt ttacctcaca ctgaatgaaa caatgataac 1276
293 taatgtaaca ttaaatataa taaaggtaat atcaacttcg taaatgcaaa aaaaaaaaaa 1336
294 aaaaaaaaaa aaaa 1350
296 <210> SEQ ID NO: 11
297 <211> LENGTH: 18
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: PCR Primer
304 <400> SEQUENCE: 11
305 ggcggaactgg acatgctt 18
307 <210> SEQ ID NO: 12
308 <211> LENGTH: 22
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: PCR Primer
316 <400> SEQUENCE: 12
317 gagtggatgt cgatcatggaa ga 22
319 <210> SEQ ID NO: 13
320 <211> LENGTH: 31
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/511,832

DATE: 10/29/2004

TIME: 11:33:34

Input Set : A:\ISIS0048-100.SEQ.txt

Output Set: N:\CRF4\10292004\J511832.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date